

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:48:45 ; Search time 4.75152 Seconds

(without alignments)
1133.013 Million cell updates/sec

Title: US-09-988-971-2_COPY_35_90

Perfect score: 288

Sequence: 1 ATAAVALGSPAGAPALSLR.....VLSEVSGREYNIPSHVAKV 56

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	35.1	512	1 I56160	protein-tyrosine k
2	101	35.1	512	1 A39719	protein-tyrosine k
3	100	34.7	505	2 I37206	protein-tyrosine k
4	99	34.4	281	2 A57152	src-like adaptor p
5	97	33.7	499	1 A40092	protein-tyrosine k
6	95	33.0	512	1 TVHUTL	protein-tyrosine k
7	92.5	32.1	512	1 B34104	protein-tyrosine k
8	90.5	31.4	509	1 TVHAST	protein-tyrosine k
9	90	31.2	503	1 UQ1321	protein-tyrosine k
10	89.5	31.1	532	1 TVHUCB	protein-tyrosine k
11	89.5	31.1	532	1 A34104	protein-tyrosine k
12	89.5	31.1	2415	1 A33733	spectrin alpha cha
13	89	30.9	507	1 A39939	protein-tyrosine k
14	88	30.6	503	1 TVMSHC	protein-tyrosine k
15	88	30.6	509	1 OKHTTK	protein-tyrosine k
16	88	30.6	509	1 I48845	protein-tyrosine k
17	87.5	30.4	526	1 TVFVR	protein-tyrosine k
18	87.5	30.4	526	1 OKFYR	protein-tyrosine k
19	87.5	30.4	526	1 S15582	protein-tyrosine k
20	87.5	30.4	526	2 S20808	protein-tyrosine k
21	87.5	30.4	533	1 TVCHS	protein-tyrosine k
22	87.5	30.4	557	1 TVFVS2	protein-tyrosine k
23	87.5	30.4	557	1 TVFVS1	protein-tyrosine k
24	87.5	30.4	568	1 TVFVPR	protein-tyrosine k
25	86.5	30.0	537	1 A45501	protein-tyrosine k
26	85.5	29.7	537	2 I51592	protein-tyrosine k
27	85.5	29.7	539	2 B49114	protein-tyrosine k
28	85.5	29.7	1113	1 A47106	myosin heavy chain
29	84.5	29.3	543	1 TVHUTS	protein-tyrosine k

30	83.5	29.0	534	1 A44991	protein-tyrosine k
31	83.5	29.0	537	1 TVHUTS	protein-tyrosine k
32	83	28.8	228	2 S25730	SH2-SH3 protein se
33	82.5	28.6	468	2 S46791	hypothetical prote
34	82.5	28.6	528	1 TVFV93	protein-tyrosine k
35	82.5	28.6	537	1 A43806	protein-tyrosine k
36	82.5	28.6	541	1 A43610	protein-tyrosine k
37	82.5	28.6	541	1 TVCHVS	protein-tyrosine k
38	82.5	28.6	542	1 TVHUSC	protein-tyrosine k
39	82.5	28.6	2429	1 SHUA	spectrin alpha cha
40	81.5	28.3	451	2 S58653	hypothetical prote
41	81.5	28.3	536	2 S33569	protein-tyrosine k
42	81.5	28.3	545	2 S52313	protein-tyrosine k
43	81.5	28.3	546	2 S52314	protein-tyrosine k
44	81.5	28.3	2427	2 T16313	hypothetical prote
45	80.5	28.0	526	1 TVFV60	protein-tyrosine k

ALIGNMENTS

RESULT 1

I56160 protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - rat

N.Contains: protein-tyrosine kinase lyn, splice form B

C.Species: Rattus norvegicus (Norway rat)

C.Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #ext_change 18-Feb-2000

C.Accession: I56160, I67811, I67812

R.Minoguchi, K.; Nishikata, H.; Sireganian, R.P.

J. Immunol. 150, 222, 1993

A.Title: Bacterially expressed rat p56lyn binds several proteins in rat basophilic leuk

A.Accession: I56160

A>Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-512 <MIN>

A.Cross-references: GB:I14951; NID:9294582; PIDN:AAA41549.1; PID:9294583

R.Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.

Gene 138, 219-222, 1994

A.Title: The cDNAs encoding two forms of the lyn protein tyrosine kinase are expressed i

A.Reference number: I53715; NID:94171041; PMID:8125304

A.Accession: I67811

A>Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-230, 'L', 232-307, 'A', 309-418, 'Y', 420-512 <RID1>

A.Cross-references: GB:I14782; NID:9294578; PIDN:AAA20944.1; PID:9294579

A.Note: in Genbank entry R4TLVNTYR, release 116.0, the source is desig

A.Accession: I67812

A>Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-24, 46-230, 'L', 232-307, 'A', 309-418, 'Y', 420-512 <RID2>

A.Cross-references: GB:I14823; NID:9294580; PIDN:AAA20945.1; PID:9294581

A.Note: in Genbank entry R4TLVNTYR, release 116.0, the source is desig

C.Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C.Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; 11pore

F.2-512/Product: protein-tyrosine kinase lyn, splice form A #status predicted <MTA>

F.2-24, 46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <MTA>

F.70-118/Domain: SH3 homology <SH3>

F.122-226/Domain: SH2 homology <SH2>

F.245-504/Domain: protein kinase homology <KIN>

F.253-261/Region: protein kinase ATP-binding motif

F.2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F.275/Active site: lys #status predicted

F.397, 508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 35.1%; Score 101; DB 1; Length 512;

Best Local Similarity 43.4%; Pred. No. 0.00069; Matches 23; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

Qy 4 VALGSPAGAPALSLRLGSPITIVSEDDGWTVLSEVSGREYNIPSHVAKV 56
Db 69 VALVYDGIHPDDLSFKKGKMKVLEHGEWMMKAKSLSSKRGFIIPSHVAKV 121

RESULT 2

A39719
protein-tyrosine kinase (EC 2.7.1.112) lym, long splice form - mouse
N/Contents: protein-tyrosine kinase lym, short splice form
C/Species: Mus musculus (house mouse)
C/Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 03-Mar-2000
A/Accession: A39719; B39719; A39750
R/Stanley, E.; Ralph, S.; McEwen, S.; Boulter, I.; Holtzman, D.A.; Lock, P.; Dunn, A.R.
Mol. Cell. Biol. 11, 3399-3406, 1991
A/Title: Alternatively spliced murine lym mRNAs encode distinct proteins.
A/Reference number: A39719; MUID:91260688; PMID:1710766
A/Accession: A39719

A/Molecule type: mRNA
A/Residues: 1-512 <STAI>
A/Cross-references: GB:M64608; NID:G198938; PIDN:AAA39470.1; PID:G198939
A/Accession: B39719
A/Molecule type: mRNA
A/Residues: 1-24,46-512 <STRA2>
A/Cross-references: GB:M64608
R/Yi, T.; Bolen, J.B.; Ihle, J.N.
Mol. Cell. Biol. 11, 2391-2398, 1991
A/Title: Hematopoietic cells express two forms of lym kinase differing by 21 amino acids
A/Reference number: A39750; MUID:91203857; PMID:2017160
A/Accession: A39750

A/Molecule type: mRNA
A/Residues: 1-76,'F',78-160,'I',162-278,'L',280-390,'I',392-424,'D',426-512 <YII>
A/Cross-references: GB:M57696; NID:G198940; PIDN:AAA39471.1; PID:G198941
A/Accession: B39750

A/Molecule type: mRNA
A/Residues: 1-24,46-76,'F',78-160,'I',162-278,'L',280-390,'I',392-424,'D',426-512 <YI2>
A/Cross-references: GB:M57697; NID:G198942; PIDN:AAA39472.1; PID:G198943
C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH3 h
C/Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
F/1-512/Product: protein-tyrosine kinase lym, long splice form #status predicted <MATR>
F/1-24,46-512/Product: protein-tyrosine kinase lym, short splice form #status predicted
F/70-118/Domain: SH3 homology <SH3>
F/129-226/Domain: SH2 homology <SH2>
F/245-504/Domain: protein kinase homology <KIN>
F/253-261/Region: protein kinase ATP-binding motif
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/275/Active site: Lys #status predicted
F/397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 35.1%; Score 101; DB 1; Length 512;
Best Local Similarity 43.4%; Pred. No. 0.00069;
Matches 23; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

Oy 4 VALGSPAGPAELSLRLGEPITVSEDDGWTWVLSVSGREYNIPSVYAKV 56
Db 69 VALPYDGIHPDLSLFFKGGKMKVLEHGEWMAKAKSLSKREGFIPSNYAKV 121

RESULT 3

I37206
protein-tyrosine kinase (EC 2.7.1.112) blk - human

C/Species: Homo sapiens (man)
C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 04-Mar-2000
A/Accession: I37206; S51647
R/Islam, K.B.; Rabbani, H.; Larsson, C.; Sanders, R.; Smith, C.I.
J. Immunol. 154, 1265-1272, 1995
A/Title: Molecular cloning, characterization, and chromosomal localization of a human ly
A/Reference number: I37206; MUID:95123078; PMID:7822795
A/Accession: I37206
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-505 <RBS>
A/Cross-references: EMBL:Z33998; NID:G601951; PIDN:CAA83965.1; PID:G601952
C/Genetics:

A/Genes: GDB:BLK
A/Cross-references: GDB:454114; OMIM:191305
A/Map position: 8p23-8p22
C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C/Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; tyro
F/65-113/Domain: SH3 homology <SH3>
F/124-220/Domain: SH2 homology <SH2>
F/239-497/Domain: protein kinase homology <KIN>
F/247-255/Region: protein kinase ATP-binding motif
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/269/Active site: Lys #status predicted

Query Match 34.7%; Score 100; DB 2; Length 505;
Best Local Similarity 41.5%; Pred. No. 0.00089;
Matches 22; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

Oy 4 VALGSPAGPAELSLRLGEPITVSEDDGWTWVLSVSGREYNIPSVYAKV 56
Db 64 VALDYTRANDRDQLWKLGEKLVKKTGDMILASLVTKGEGVPSNFAKV 116

RESULT 4

A57152
src-like adaptor protein - mouse

C/Species: Mus musculus (house mouse)
C/Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 12-Feb-1999
A/Accession: A57152
R/Pandey, A.; Duan, H.; Dixit, V.M.
J. Biol. Chem. 270, 19201-19204, 1995
A/Title: Characterization of a novel Src-like adaptor protein that associates with the E
A/Reference number: A57152; MUID:95370243; PMID:7543898
A/Accession: A57152

A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-281 <PAN>
A/Cross-references: GB:U29056
C/Superfamily: SH3 homology; SH2 homology
F/29-77/Domain: SH3 homology <SH3>
F/94-175/Domain: SH2 homology <SH2>

Query Match 34.4%; Score 99; DB 2; Length 281;
Best Local Similarity 37.3%; Pred. No. 0.00062;
Matches 19; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Oy 6 LQSPFAGPAELSLRLGEPITVSEDDGWTWVLSVSGREYNIPSVYAKV 56
Db 30 LNDVPSDDISPIFRGKELRVISDEGWMKALISGRRESYIGICVAKV 80

RESULT 5

A40092
protein-tyrosine kinase (EC 2.7.1.112) blk (validated) - mouse

C/Species: Mus musculus (house mouse)
C/Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000
A/Accession: A40092
R/Dymecki, S.M.; Niederhuber, J.E.; Desiderio, S.V.
Science 247, 332-336, 1990
A/Title: Specific expression of a tyrosine kinase gene, blk, in B lymphoid cells.
A/Reference number: A40092; MUID:90117147; PMID:2404338
A/Accession: A40092

A/Molecule type: mRNA
A/Residues: 1-499 <DTM>
A/Cross-references: GB:M30903; NID:G202076; PIDN:AAA40453.1; PID:G202077
C/Genetics:
A/Genes: MGI:BLK
A/Cross-references: MGI:88169
A/Map position: 14:28.0
C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F/118-214/Domain: SH3 homology <SH3>
F/59-107/Domain: SH2 homology <SH2>
F/233-491/Domain: protein kinase homology <KIN>
F/241-249/Region: protein kinase ATP-binding motif
F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F/263/Active site: Lys #status predicted

Query Match 33.7%; Score 97; DB 1; Length 499;
A/Accession: A40092

[illegible]

F:1977-1024/DomAin: SH3 homology <SH3>
F:1977-1024/DomAin: spectrin/dystrophin repeat homology <SP10>
F:1180-1285/DomAin: spectrin/dystrophin repeat homology <SP11>
F:1186-1381/DomAin: spectrin/dystrophin repeat homology <SP12>
F:1192-1497/DomAin: spectrin/dystrophin repeat homology <SP13>
F:1198-1604/DomAin: spectrin/dystrophin repeat homology <SP14>
F:1605-1710/DomAin: spectrin/dystrophin repeat homology <SP15>
F:1711-1816/DomAin: spectrin/dystrophin repeat homology <SP16>
F:1817-1922/DomAin: spectrin/dystrophin repeat homology <SP17>
F:1923-2029/DomAin: spectrin/dystrophin repeat homology <SP18>
F:2038-2143/DomAin: spectrin/dystrophin repeat homology <SP19>
F:2152-2252/DomAin: spectrin/dystrophin repeat homology <SP20>
F:2265-2297/DomAin: calmodulin repeat homology <EF1>
F:2308-2340/DomAin: calmodulin repeat homology <EF2>

Query Match 31.1%; Score 89.5; DB 1; Length 2415;
Best Local Similarity 35.2%; Pred. No. 0.079;
Matches 19; Conservative 15; Mismatches 17; Indels 3; Gaps 2;

OY 4 VALGSPAGPAELSLRLGEPLTIV-SEDDGMWTVLSEVSGREYNIPSVHAKV 56
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 976 VALDYETPHDGDGLKQGEKLVLVEESGEWMRAQSITTGDEGLPIHNFMVMV 1027

RESULT 13
A39939
protein-tyrosine kinase (EC 2.7.1.112) tk1 [similarity] - chicken
N:Alternate names: kinase-related transforming protein (tk1); T-cell surface antigen associated protein (tk1)
C:Date: 16-Jun-2000 #sequence__revision 16-Jun-2000 #text_change 16-Jun-2000
R:Accession: A42126; A39939
S:Chow, L.M.; Ratcliffe, M.J.; Veillette, A.
Mol. Cell. Biol. 12, 1226-1233, 1992
A:Title: tk1 is the avian homolog of the mammalian lck tyrosine protein kinase gene.
A:Reference number: A42126; PMID:92186854; PMID:1545804
A:Accession: A42126
A:Molecule type: mRNA
A:Residues: 1-88 <CHO>
A:Cross-references: GB:W85043
A:Experimental source: thymus, spleen
A>Note: sequence extracted from NCBI Backbone (NCBIN:88831, NCBIP:88833)
R:Strehardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987
A:Title: Additional member of the protein-tyrosine kinase family: the src-and lck-related A:Reference number: A39939; PMID:8609370; PMID:3321053
A:Accession: A39939
A:Molecule type: mRNA
A:Residues: 52-507 <STR>
A:Cross-references: GB:U03579; NID:9212712; PIDN:AAA49081.1; PID:9212713
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology; ATP autophosphorylation; blocked amino end; lipoprotein; myristylation; pnc F:66-114/DomAin: SH3 homology <SH3>
F:125-222/DomAin: SH2 homology <SH2>
F:241-499/DomAin: protein kinase homology <Kin>
F:249-557/Region: protein kinase ATP-binding motif
F:250/Modified site: myristylated amino end (Gly) (n mature form) #status predicted F:392/Motif site: phosphorylated (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 30.9%; Score 89; DB 1; Length 507;
Best Local Similarity 37.7%; Pred. No. 0.017;
Matches 20; Conservative 8; Mismatches 25; Indels 0; Gaps 0;

OY 4 VALGSPAGPAELSLRLGEPLTIVSEDDGMWTVLSEVSGREYNIPSVHAKV 56
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 65 VALDYETPHDGDGLKQGEKLVLVEESGEWMRAQSITTGDEGLPIHNFMVMV 117

RESULT 14
TYMSHC
protein-tyrosine kinase (EC 2.7.1.112) hck - mouse
N:Alternate names: Kinase-related transforming protein (bnk)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1989 #sequence__revision 31-Dec-1989 #text_change 28-Jan-2000

C:Accession: A27282; A39973
 R:Klemz, M.J.; McKechar, S.R.; Maki, R.A.
 Nucleic Acids Res. 15, 9600, 1987
 A:Title: Nucleotide sequence of the mouse hck gene.
 A:Reference number: A27282; MUID:88067781; PMID:3684607
 A:Accession: A27282
 A:Molecule type: mRNA
 A:Residues: 1-503 <KLE>
 A:Cross-references: GB:Y00487; NID:951209; PIDN:CAA68544.1; PID:951210
 R:Holtzman, D.A.; Cook, W.D.; Dunn, A.R.
 Proc. Natl. Acad. Sci. U.S.A. 84, 8325-8329, 1987
 A:Title: Isolation and sequence of a cDNA corresponding to a src-related gene expressed
 A:Reference number: A39973; MUID:88068589; PMID:3317404
 A:Accession: A39973
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-503 <HOL>
 A:Cross-references: GB:J03023; NID:9192212; PIDN:AAA37305.1; PID:9309118
 C:Genetics:
 A:Gene: hck
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
 F:62-110/Domain: SH3 homology <SH3>
 F:121-218/Domain: SH2 homology <SH2>
 F:237-495/Domain: protein kinase homology <KIN>
 F:245-253/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3/Binding site: palmitate (Cys) (covalent) #status predicted
 F:267/Active site: Lys #status predicted
 F:388,499/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 30.6%; Score 88; DB 1; Length 503;
 Best Local Similarity 35.8%; Pred. No. 0.022;
 Matches 19; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

Oy 4 VALGSPAGPAPLRLRGEPLTIVSEDDGMWTVLSEVSGENNIPSHVAKV 56
 Db 61 VALDYEAHREDSPQKGDQWVLEBAGEMWKRSLATKEGYIPSNVAVRV 113

RESULT 15
 OKHOLK
 protein-tyrosine kinase (EC 2.7.1.112) lck - human
 N:Alternate names: kinase-related transforming protein (lck)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 28-Jan-2000
 C:Accession: J00152; S07822; S07200; S01879; S07143; A32787; I57636
 R:Rouer, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R.
 Gene 84, 105-113, 1989
 A:Title: Structure of the human lck gene: differences in genomic organisation within src
 A:Reference number: J00152; MUID:90108697; PMID:2558056
 A:Accession: J00152
 A:Molecule type: DNA
 A:Residues: 1-509 <ROU>
 A:Cross-references: EMBL:X14053
 R:Perlmuter, R.M.; March, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.
 J. Cell. Biochem. 38, 117-126, 1988
 A:Title: Structure and expression of lck transcripts in human lymphoid cells.
 A:Reference number: S07822; MUID:89123626; PMID:3365417
 A:Accession: S07822
 A:Molecule type: mRNA
 A:Residues: 1-86; 'P', 88-509 <PER>
 A:Cross-references: EMBL:X13529; NID:934294; PIDN:CAA31884.1; PID:934295
 R:Koga, Y.; Cacciat, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikaki, Y.; Mak, T.W.
 Eur. J. Immunol. 16, 1643-1646, 1986
 A:Title: A human T cell-specific cDNA clone (YTI6) encodes a protein with extensive homc
 A:Reference number: S07200; MUID:87133831; PMID:3493153
 A:Accession: S07200
 A:Molecule type: mRNA
 A:Residues: 1-205; 'ASAIRPI', 212-257; 'RCGW', 262; 'TTT', 266; 'T', 268-281; 'AGRLP', 287-503; 'ST
 A:Cross-references: EMBL:X05027; NID:936807; PIDN:CAA28691.1; PID:936808
 R:Veilleux, A.; Rose, F.M.; Sauvillie, E.A.; Bolen, J.B.; Rosen, N.
 Oncogene Res. 1, 357-374, 1987

A:Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other n
 A:Reference number: S01879; MUID:88217332; PMID:2835736
 A:Accession: S01879
 A:Molecule type: mRNA
 A:Residues: 368-471; 'H', 473-509 <VEI>
 A:Cross-references: EMBL:X06569; NID:934289; PIDN:CAA29667.1; PID:934289
 R:Trevisan, U.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canina, C.; Lima, T.J.
 Biochem. Biophys. Acta 888, 286-295, 1986
 A:Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56 (LSTRA).
 A:Reference number: S07143; MUID:87000726; PMID:3489486
 A:Accession: S07143
 A:Molecule type: mRNA
 A:Residues: 'A', 376-509 <TRE>
 A:Cross-references: EMBL:X04476; NID:935779; PIDN:CAA28165.1; PID:935780
 R:Takadera, T.; Leung, S.; Geronne, A.; Koga, Y.; Takahara, Y.; Miyamoto, N.G.; Mak, T.W.
 Mol. Cell. Biol. 9, 2173-2180, 1989
 A:Title: Structure of the two promoters of the human lck gene: differential accumulation
 A:Reference number: A32797; MUID:89313764; PMID:2787474
 A:Accession: A32797
 A:Molecule type: DNA
 A:Residues: 1-35 <TKA>
 A:Cross-references: GB:M26692; NID:9341523; PIDN:AAA59503.1; PID:9349702
 R:Garvin, A.M.; Pauer, S.; March, J.D.; Perlmuter, R.M.
 Mol. Cell. Biol. 8, 3058-3064, 1988
 A:Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cell
 A:Reference number: I57636; MUID:89096891; PMID:2850479
 A:Accession: I57636
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-35; 'VR' <RES>
 A:Cross-references: GB:M2510; NID:9187031; PIDN:AAA59501.1; PID:9553522
 C:Comment: Protein tyrosine kinases play important roles in the control of cell growth a
 C:Genetics:
 A:Gene: GDB:LCR
 A:Cross-references: GDB:119360; OMIM:153390
 A:Map position: 1p35-1p34.3
 A:Introns: 35/3; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
 C:Function:
 A:Description: catalyzes the phosphorylation of a peptide tyrosine residue by ATP
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
 F:2-509/Product: protein-tyrosine kinase lck #status predicted <MAT>
 F:68-116/Domain: SH3 homology <SH3>
 F:127-224/Domain: SH2 homology <SH2>
 F:243-501/Domain: protein kinase homology <KIN>
 F:251-259/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3/Binding site: palmitate (Cys) (covalent) #status predicted
 F:273/Active site: Lys #status predicted
 F:394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 30.6%; Score 88; DB 1; Length 509;
 Best Local Similarity 36.5%; Pred. No. 0.022;
 Matches 19; Conservative 8; Mismatches 25; Indels 0; Gaps 0;

Oy 4 VALGSPAGPAPLRLRGEPLTIVSEDDGMWTVLSEVSGENNIPSHVAKV 55
 Db 67 IALHSYPSHSDGLGFEKGBQRLIBOSGEMWKRSLATKEGYIPSNVAVRV 118

Search completed: March 24, 2003, 15:51:40
 Job time: 5.75152 secs